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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/589,328	08/14/2006	Byung Ok Choi	CHOI ET AL-1 PCT	3922

25889 7590 09/10/2008

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EXAMINER	
PANDE, SUCHIRA	
ART UNIT	PAPER NUMBER
1637	
MAIL DATE	DELIVERY MODE
09/10/2008	PAPER

Please find below and/or attached an Office communication concerning this application or proceeding.

The time period for reply, if any, is set in the attached communication.

Office Action Summary	Application No.	Applicant(s)	
	10/589,328	OK CHOI ET AL.	
	Examiner	Art Unit	
	SUCHIRA PANDE	1637	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☐ Responsive to communication(s) filed on _____.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-5* is/are pending in the application.

4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☐ Claim(s) _____ is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☒ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☒ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO/SB/08) Paper No(s)/Mail Date *8/14/06;11/22/06*.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____.
5) ☐ Notice of Informal Patent Application
6) ☐ Other: _____.

DETAILED ACTION

Priority

1. Receipt is acknowledged of papers submitted under 35 U.S.C. 119(a)-(d), which papers have been placed of record in the file. This is a national stage application of PCT/KR05/002170 filed on July 6, 2005. Applicant has claimed priority to Parent Korean application KR 10-2004-0052652 filed on July 7, 2004, however no English translation of this certified Korean Document is provided. Accordingly for search purposes the priority date of the instant application is same as the filing date of PCT application which is July 6, 2005.

Information Disclosure Statement

2. The information disclosure statement (IDS) submitted on August 14, 2006 and November 22, 2006 is in compliance with the provisions of 37 CFR 1.97. Accordingly, the information disclosure statement is being considered by the examiner.

Claim Rejections - 35 USC § 112

3. The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

4. Claims 1-5 are rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for diagnosis an inherited neuropathies caused by duplication or deletion of a region located in chromosome 17 that result in CMTIA and HNPP does not reasonably provide enablement for diagnosis of all types of inherited neuropathies. In addition, the specification as filed is enabled for diagnosis an inherited

neuropathies requiring use of at least three markers from the six markers recited. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to use the invention commensurate in scope with these claims. The claims as recited are very broad. Currently claim 1 as recited is not drawn to simultaneous detection of at least 3 markers.

There are many factors to be considered when determining whether there is sufficient evidence to support a determination that a disclosure does not satisfy the enablement requirement and whether any necessary experimentation is "undue." These factors include, but are not limited to:

(A) The breadth of the claims;

The claims are broad and encompass diagnosis of all types of inherited neuropathies. However the specification as well as markers used for PCR amplification is only suitable for diagnosis of the inherited neuropathies caused by either duplication or deletion of micro satellite region present in chromosome 17p11.2-p12. The duplication of region results in CMT1A and deletion results in HNPP.

No guidance is provided to one of ordinary skill in the art how other types of inherited neuropathies that are caused by genes located in chromosome 1, sex chromosomes and other locations can be diagnosed using the claimed invention.

(B) The nature of the invention;

The invention is related to diagnosis of inherited neuropathy using molecular biology techniques to detect duplication or deletion of a region located in chromosome 17 that encodes a gene for PMP22 (peripheral myelin protein 22). PCR amplification of

micro satellites in the region is performed to determine the number of copies of the region present in the sample obtained from patient. If only 2 copies are present the subject is normal. Three copies of the region due to duplication results in CMT1A and only one copy of the region due to deletion results in patients having HNPP.

(C) The state of the prior art;

Prior art suggests the existence of many different kinds of inherited neuropathies (see review by Suter et al. 2003). There are many types of Charcot-Marie-Tooth Disease (CMT). The CMT Type 1A locus maps to human chromosome 17 (region p11-p12); the CMT1B locus maps to human chromosome 1 (region q23-q25) and a third type is unlinked to both the CMT1A and CMT1B loci (see par. 2 on page 219 in Lupski et al. Cell 1991 vol. 66: 219-232). Besides these there are many others types of inherited neuropathies listed in Table 1 of review written by Suter et al. (2003) Nature Reviews /Neuroscience vol. 4 pp 714-726.

(D) The level of one of ordinary skill;

The level of one of ordinary skill in the art is high as average biomedical worker is fully trained with all the supervisors generally having a PhD. The clinicians working in the area of human genetics generally have dual MD/PhD degrees with lots of research and data interpretation experience

(E) The level of predictability in the art;

The specification provides guidance regarding how to diagnose the inherited neuropathy that is caused by duplication or deletion of mirosatellites found in chromosome 17 by performing PCR with the provided PCR markers and correlating the

results with the large pedigree analysis. Such diagnostic conclusions can only be drawn, when the location of the underlying genetic mutation is well documented in human chromosome. The location must be known at the DNA sequence level that is the sequence of molecular markers flanking the mutation sites is known. Furthermore a perfect correlation must be known to exist between various genotypes and corresponding phenotypes (normal, carrier and disease phenotype). When this scenario exists then its possible that perhaps PCR based tests can be designed to unambiguously diagnose the disease.

(F) The amount of direction provided by the inventor;

Since no guidance is provided in the specification regarding what is the exact underlying cause of the CMT1B and the third type of inherited neuropathy along with the different neuropathies listed in the Table 1 of Suter et al. Then one of ordinary skill is not given guidance which markers to use and how to go about detecting the correlation between those markers and the other types of inherited neuropathies that are known to be present in humans.

Page 9 lines 13-23 clearly indicate that simultaneous diagnosis of 3 markers D17S9B, D17S9A and D17S918 (Triplex PCR) is minimally required to obtain 97.5% accuracy of diagnosis while use of all 6 markers improves the accuracy of diagnosis to 99.96 %. The diagnosis can be performed in a sequential manner two step manner involving Triplex PCR and using the remaining 3 markers if it is difficult to make definitive diagnosis. Thus as per the specification the method minimally requires

diagnosis of at least 3 markers simultaneously. However claim 1 does not recite this requirement.

(G) The existence of working examples;

The working examples provided are related to detection and diagnosis of inherited neuropathy due to alteration of a region in chromosome 17. No information at all is provided for CMT1B and other known inherited neuropathies taught by prior art.

(H) The quantity of experimentation needed to make or use the invention

Based on the content of the disclosure, one of ordinary skill would have to figure out whether a correlation exists between detection of a marker on chromosome 1 and diagnosis of CMT1B since CMT1B locus maps to human chromosome 1 (region q23-q25). But for the inherited neuropathies that are unlinked to both CMT1A and CMT1B, one of ordinary skill does not even have a clue as to what is the genetic cause that results in this third type of inherited neuropathy, whether it's a polygenic trait or how to go about detecting it. Thus the amount of experimentation needed to make or use the invention will be enormous. Furthermore there is no certainty that after lot of experimentation one of ordinary skill will be successful in diagnosing CMT1B and all the other types of inherited neuropathies known. Thus Examiner concludes that undue experimentation is required on the part of one of ordinary skill. For each specific disease the marker would have to be identified and even after that there is no guarantee that they could diagnose all the various types of inherited neuropathies using multiplex PCR with 6 markers. See In re Wands, 858 F.2d 731, 737, 8 USPQ2d 1400, 1404 (Fed. Cir. 1988).

The test of enablement is whether one reasonably skilled in the art could make or use the invention from the disclosures in the patent coupled with information known in the art without undue experimentation. Hence Examiner reaches the conclusion that the specification as filed is not enabled for diagnosis of *all types of inherited neuropathies* claimed. The specification is enabled for diagnosis of CMTIA and HNPP using the six markers identified by applicant. This is a scope of enablement rejection.

Claim Interpretation

5. Table in the specification lists a correspondence between a pair of primers claimed and the marker it corresponds to. Based on this information primers of

SEQ ID NOs 1 and 2 identify marker D17S921 on chromosome 17

SEQ ID NOs 3 and 4 identify marker D17S9B on chromosome 17

SEQ ID NOs 5 and 6 identify marker D17S9A on chromosome 17

SEQ ID NOs 7 and 8 identify marker D17S918 on chromosome 17

SEQ ID NOs 9 and 10 identify marker D17S2230 on chromosome 17

SEQ ID NOs 11 and 12 identify marker D17S4A on chromosome 17.

Prior art teaches sequences that are 100% identical to claimed SEQ ID nos. These sequences are located on human chromosome 17. Only D17S921 on chromosome 17 is labeled as such in prior art. Remaining 5 markers are not identified by the nomenclature used in the instant application in prior art. Examiner has not found any teaching in the prior art where these six markers have been used to diagnose the inherited neuropathies specifically CMTIA and HNPP. Hence the use of these markers for diagnosis of CMT1A and HNPP is novel.

Closest Prior art Found by Examiner related to the claimed invention

6. Thiel et al. (2002) European Journal of Human Genetics vol. 11: pp 170-178; Gyapay et al. (1994) Nature Genetics vol. 7 pp 246-339; Birren et al. (1999) accession nos AC013248, Birren et al. (2000) accession nos AC005703; Birren et al. (2001) accession no AC005517 direct submission by Whitehead Institute/MIT Center for Genome Research to Genebank; Gerken et al. Am. J. Hum. Genet. 56 (2), 484-499 (1995); and Ota et al. (2003) accession no BD155303 direct submission to Gene Bank.

Thiel et al. teach a method for diagnosing an inherited neuropathy (see page 170 par. 1 where CMTIA and HNPP two inherited neuropathies are taught) but do not teach wherein PCR amplification is carried out using the 6 loci of chromosome 17 recited namely: D17S921, D17S9B, D17S9A, D17S918, D17S2230 and D17S4A as markers.

Gyapay et al. teach marker D17S921 (see page 319 of Gyapay et al. where marker D17S921 is taught. SEQ ID NO 1 of instant application is 100 identical to nucleotide 164 to nt 187 taught by Gyapay et al. as part of marker D17S921.

See alignment of SEQ ID NO 1 to sequence taught by Gyapay et al. below:

```
RESULT 1
Z23462
LOCUS       Z23462                  335 bp    DNA     linear   PRI 27-NOV-
1994
DEFINITION  H. sapiens (D17S921) DNA segment containing (CA) repeat; clone
            AFM191xh12; single read.
ACCESSION   Z23462
VERSION     Z23462.1  GI:393651
KEYWORDS    CA repeat; dinucleotide repeat; GT repeat; microsatellite DNA;
            microsatellite marker; repeat polymorphism.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
            Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Gyapay,G., Morissette,J., Vignal,A., Dib,C., Fizames,C.,
```

```
            Millasseau,P., Marc,S., Bernardi,G., Lathrop,M. and
Weissenbach,J.
  TITLE     The 1993-94 Genethon human genetic linkage map
  JOURNAL   Nat. Genet. 7 (2 SPEC NO), 246-339 (1994)
   PUBMED   7545953
  Query Match             100.0%;  Score 24;  DB 5;  Length 335;
  Best Local Similarity   100.0%;  Pred. No. 0.28;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps
0;

Qy          1 GTGTTGTATTAGGCAGAGTTCTCC 24 SEQ ID NO. 1
              ||||||||||||||||||||||||
Db        164 GTGTTGTATTAGGCAGAGTTCTCC 187
```

Alignment of SEQ ID NO 2 shows a 100 % match with sequence with region 310 to 287 of marker D17S921 taught by Gyapay et al.

```
ORIGIN

  Query Match             100.0%;  Score 24;  DB 5;  Length 335;
  Best Local Similarity   100.0%;  Pred. No. 15;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps
0;

Qy          1 GGCAGTAGATGGTGACTTTATGGC 24 SEQ ID NO. 2
              ||||||||||||||||||||||||
Db        310 GGCAGTAGATGGTGACTTTATGGC 287
```

Regarding claims 1-5, Birren et al. (1999) teach the sequence on chromosome 17 clone RP11-64B12 that shows 100% match to SEQ ID NO 3 through SEQ ID NO 6 of instant claims.

Sequences 2187 to 2211 are identical to SEQ ID NO 3

Sequences 2301 to 2281 are identical to SEQ ID NO 4.

Sequences 24319 to 24344 are identical to SEQ ID NO 5.

Sequences 24502 to 24480 are identical to SEQ ID NO 6

See alignments below

```
AC013248
LOCUS       AC013248               66571 bp    DNA     linear   PRI 30-DEC-
1999
DEFINITION  Homo sapiens chromosome 17, clone RP11-64B12, complete sequence.
ACCESSION   AC013248
VERSION     AC013248.5  GI:6648218
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
            Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 66571)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C. and Lander,E.
  TITLE     Homo sapiens chromosome 17, clone RP11-64B12
  TITLE     Direct Submission
  JOURNAL   Submitted (30-DEC-1999) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT     On Dec 30, 1999 this sequence version replaced gi:6634866.
            All repeats were identified using RepeatMasker:
            Smit, A.F.A. & Green, P. (1996-1997)
            http://ftp.genome.washington.edu/RM/RepeatMasker.html
  Query Match           100.0%;  Score 25;  DB 5;  Length 66571;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps
0;

Qy          1 TCTCAGTCCTGATTTCTTGATTTTG 25  SEQ ID NO 3
              |||||||||||||||||||||||||
Db       2187 TCTCAGTCCTGATTTCTTGATTTTG 2211


  Query Match           100.0%;  Score 21;  DB 5;  Length 66571;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps
0;

Qy          1 CCAGAGCTAACACCACATTCA 21   SEQ ID NO 4
              |||||||||||||||||||||
Db       2301 CCAGAGCTAACACCACATTCA 2281

Query Match           100.0%;  Score 26;  DB 5;  Length 66571;
  Best Local Similarity   100.0%;  Pred. No. 0.24;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps
0;

Qy          1 CAACCATCAGTGATTTGATGGTTTAC 26 SEQ ID NO 5
              ||||||||||||||||||||||||||
Db      24319 CAACCATCAGTGATTTGATGGTTTAC 24344



  Query Match           100.0%;  Score 23;  DB 5;  Length 66571;
```

```
  Best Local Similarity   100.0%;  Pred. No. 0.073;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps
0;

Qy          1 GAGTTGTCACTAGAACCCTGTTC 23  SEQ ID NO 6
              |||||||||||||||||||||||
Db      24502 GAGTTGTCACTAGAACCCTGTTC 24480
```

Birren et al. (2000) teach the sequence on chromosome 17 clone hRPK.849_N_15 that shows 100% match to SEQ ID NO 7, SEQ ID NO 11 and SEQ ID NO 12 of instant claims.

Sequences 173907 to 173930 are identical to SEQ ID NO 7.

Sequences 162166 to 162189 are identical to SEQ ID NO 11.

Sequences 162327 to 162304 are identical to SEQ ID NO 12.

See alignment below

```
AC005703
LOCUS       AC005703              233454 bp    DNA     linear   PRI 09-MAY-
2000
DEFINITION  Homo sapiens chromosome 17, clone hRPK.849_N_15, complete
sequence.
ACCESSION   AC005703
VERSION     AC005703.2  GI:7740042
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
            Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 233454)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C. and Lander,E.
  TITLE     Homo sapiens chromosome 17, clone hRPK.849_N_15
  JOURNAL   Unpublished
  TITLE     Direct Submission
  JOURNAL   Submitted (24-SEP-1998) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA

  Query Match             100.0%;  Score 24;  DB 5;  Length 233454;
  Best Local Similarity   100.0%;  Pred. No. 0.42;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps
0;
```

```
Qy          1 TCCTGTAATCTGTCCCCAAACGTC 24  SEQ ID NO 7
              ||||||||||||||||||||||||
Db     173907 TCCTGTAATCTGTCCCCAAACGTC 173930


Query Match             100.0%;  Score 24;  DB 5;  Length 233454;
  Best Local Similarity   100.0%;  Pred. No. 0.84;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps
0;

Qy          1 CTGTGGAGGAAAGAAAACACTGCC 24  SEQ ID NO 11
              ||||||||||||||||||||||||
Db     162166 CTGTGGAGGAAAGAAAACACTGCC 162189


  Query Match             100.0%;  Score 24;  DB 5;  Length 233454;
  Best Local Similarity   100.0%;  Pred. No. 0.098;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps
0;

Qy          1 GCACTAAAGTAGCTTGTAACTCTG 24  SEQ ID NO 12
              ||||||||||||||||||||||||
Db     162327 GCACTAAAGTAGCTTGTAACTCTG 162304
```

Gerken et al. (1995) teach the sequence on chromosome 17 STS UT1860 that shows 100% match to SEQ ID NO 8 of instant claims.

Sequences 316 to 292 taught by Gerken et al. are identical to SEQ ID NO 8.

Sequences 297 to 316 are taught as the primer binding site by Gerken et al.

See alignment below :

```
HUMUT1860/c
LOCUS       HUMUT1860                319 bp    DNA     linear   STS 31-JUL-
1995
DEFINITION  Human chromosome 17 STS UT1860, sequence tagged site.
ACCESSION   L18709
VERSION     L18709.1  GI:307808
KEYWORDS    STS; PCR primer; STS sequence; microsatellite marker;
            microsatellite repeat; repeat polymorphism; sequence tagged site.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
            Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 319)
  AUTHORS   Gerken,S.C., Matsunami,N., Lawrence,E., Carlson,M., Moore,M.,
            Ballard,L., Melis,R., Robertson,M., Bradley,P., Elsner,T.,
            Tingey,A., Rodriguez,P., Albertsen,H., Lalouel,J.-M. and White,R.
  TITLE     Genetic and physical mapping of simple sequence repeat containing
```

```
            sequence tagged sites from the human genome
  JOURNAL   Unpublished (1993)
REFERENCE   2  (bases 1 to 319)
  AUTHORS   Gerken,S.C., Albertsen,H., Elsner,T., Ballard,L., Holik,P.,
            Lawrence,E., Moore,M., Zhao,X. and White,R.
  TITLE     A strategy for constructing high-resolution genetic maps of the
            human genome: a genetic map of chromosome 17p, ordered with
meiotic
            breakpoint-mapping panels
  JOURNAL   Am. J. Hum. Genet. 56 (2), 484-499 (1995)
   PUBMED   7847385
COMMENT     Original source text: Homo sapiens.
            Submitted by: Utah Center for Human Genome Research University of
            Utah, Dept. of Human Genetics
            2160 Eccles Institute of Human Genetics
            Salt Lake City, UT  84112
            e-mail: sts@corona.med.utah.edu
            Primer A: TGTTGAGCTTTCCTGTAATC
            Primer B: TTCCTCACACAACCTATTGA
            32P-label: B Primer
            PCR Profile:
            Initial Denaturation: 94C 300sec
            PCR Cycles: 5
            Denaturation: 94C  10sec
            Annealing: 56C  10sec
            Extension: 72C  20sec
            Mg++: 1mM
            Gel: Acrylamide 7%, Formamide 32%, Urea 34%
            Alleles: 3.
FEATURES             Location/Qualifiers
     source          1. .319
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /map="17"
     STS             72. .316
                     /standard_name="STS UT1860"
     primer_bind     72. .91
     primer_bind     complement(297. .316)
ORIGIN

  Query Match             100.0%;  Score 25;  DB 7;  Length 319;
  Best Local Similarity   100.0%;  Pred. No. 37;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps
0;

Qy          1 TTCCTCACACAACCTATTGATAGTC 25
              |||||||||||||||||||||||||
Db        316 TTCCTCACACAACCTATTGATAGTC 292
```

Birren et al. (2001) teach the sequence on chromosome 17 clone RP11-726O12 accession no AC005517 that shows 100% match to SEQ ID NO 9 of instant claims.

Sequences 55299 to 55323 are identical to SEQ ID NO 9.

See alignment below

```
AC005517
LOCUS       AC005517               106210 bp    DNA     linear   PRI 03-MAR-
2001
DEFINITION  Homo sapiens chromosome 17, clone RP11-726O12, complete sequence.
ACCESSION   AC005517
VERSION     AC005517.7  GI:13194375
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
            Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 106210)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C. and Lander,E.
  TITLE     Homo sapiens chromosome 17, clone RP11-726O12
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 106210)
  AUTHORS   Birren,B.,  Query Match             100.0%;  Score 25;  DB 5;
Length 106210;
  Best Local Similarity   100.0%;  Pred. No. 0.16;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps
0;

Qy          1 AGGAAACTGATGTCTAAAACTATCC 25    SEQ ID NO 9
              |||||||||||||||||||||||||
Db      55299 AGGAAACTGATGTCTAAAACTATCC 55323
```

Ota et al. (2003) teach primers for synthesis of cDNA in accession no BD155303 that shows 100% match to SEQ ID NO 10 of instant claims.

Sequences 80 to 57 are identical to SEQ ID NO 10.

See alignment below

```
LOCUS       BD155303                396 bp    DNA     linear   PAT 17-JAN-
2003
DEFINITION  Primer for synthesizing full-length cDNA and use thereof.
ACCESSION   BD155303
VERSION     BD155303.1  GI:27861061
KEYWORDS    JP 2002191363-A/10146.
```

```
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
            Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 396)
  AUTHORS   Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K.,
Yamamoto,J.,
            Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
  TITLE     Primer for synthesizing full-length cDNA and use thereof
  JOURNAL   Patent: JP 2002191363-A 10146 09-JUL-2002;
            HELIX RESEARCH INSTITUTE
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002191363-A/10146
            PD   09-JUL-2002
            PF   28-JUL-2000 JP 2000280990
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WAKAMATSU,
            PI   KEIICHI NAGAI,TETSUJI OTSUKI
            PC
            C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/
PC
            10,
            PC   C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00
CC
            Primer for synthesizing full-length cDNA and use thereof FH   Key
            Location/Qualifiers
            FT   source          1. .396
            FT                   /organism='Homo sapiens (human)'.

  Query Match             100.0%;  Score 24;  DB 2;  Length 396;
  Best Local Similarity   100.0%;  Pred. No. 0.61;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps
0;

Qy          1 GTGAATCCAGGAGGCAGAGCTTGC 24 SEQ ID NO 10
              ||||||||||||||||||||||||
Db         80 GTGAATCCAGGAGGCAGAGCTTGC 57
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Thus sequences of regions that contain the 6 claimed marker loci were taught by prior art. However prior art has not shown use of these markers for diagnosis of inherited neuropathies. Hence the prior art does not provide any motivation or suggestion to use these specific marker sequences for diagnosis of CMTIA or HNPP as taught by Thiel et al.

Therefore the claimed set of markers for diagnosis of CMTIA or HNPP is novel.

Conclusion

Allowable Subject Matter

7. No references were found teaching or suggesting claims 1-2, but they are rejected for reasons given above.

8. Any inquiry concerning this communication or earlier communications from the examiner should be directed to SUCHIRA PANDE whose telephone number is (571)272-9052. The examiner can normally be reached on 8:30 am -5:00 pm.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Gary Benzion can be reached on 571-272-0782. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free). If you would like assistance from a USPTO Customer Service Representative or access to the automated information system, call 800-786-9199 (IN USA OR CANADA) or 571-272-1000.

Suchira Pande
Examiner
Art Unit 1637

/Teresa E Strzelecka/

Primary Examiner, Art Unit 1637

September 9, 2008